

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/096,500

OIPE

#8

DATE: 06/22/98  
TIME: 11:01:53

INPUT SET: S26845.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Ashkenazi, Avi J.  
Baker, Kevin  
Chuntharapai, Anan  
Gurney, Austin  
Kim, Kyung Jin  
Wood, William

ENTERED

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 12-Jun-1998  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911  
(B) FILING DATE: 18-JUN-1997

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.  
(B) REGISTRATION NUMBER: 35,600  
(C) REFERENCE/DOCKET NUMBER: P1110P1

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5416  
(B) TELEFAX: 650/952-9881

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/096,500DATE: 06/22/98  
TIME: 11:01:55

INPUT SET: S26845.raw

47 (2) INFORMATION FOR SEQ ID NO:1:  
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 259 amino acids

51 (B) TYPE: Amino Acid

52 (D) TOPOLOGY: Linear  
5354 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
5556 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val  
57 1 5 10 1558  
59 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg  
60 20 25 3061  
62 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg  
63 35 40 4564  
65 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser  
66 50 55 6067  
68 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr  
69 65 70 7570  
71 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val  
72 80 85 9073  
74 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg  
75 95 100 10576  
77 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn  
78 110 115 12079  
80 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu  
81 125 130 13582  
83 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val  
84 140 145 15085  
86 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu  
87 155 160 16588  
89 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu  
90 170 175 18091  
92 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu  
93 185 190 19594  
95 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu  
96 200 205 21097  
98 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu  
99 215 220 225

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/096,500DATE: 06/22/98  
TIME: 11:01:57

INPUT SET: S26845.raw

100  
101 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr  
102 230 235 240  
103  
104 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu  
105 245 250 255  
106  
107 Ile Val Phe Val  
108 259  
109

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

120  
121 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50  
122  
123 ATTTTGTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100  
124  
125 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150  
126  
127 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195  
128 Met  
129 1  
130  
131 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234  
132 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile  
133 5 10  
134  
135 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273  
136 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr  
137 15 20 25  
138  
139 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312  
140 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala  
141 30 35 40  
142  
143 CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351  
144 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys  
145 45 50  
146  
147 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390  
148 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys  
149 55 60 65  
150  
151 AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429  
152 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/096,500

 DATE: 06/22/98  
 TIME: 11:01:58

INPUT SET: S26845.raw

	70	75	
153			
154			
155	AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA	468	
156	Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys		
157	80	85	90
158			
159	TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA	507	
160	Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg		
161	95	100	105
162			
163	GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT	546	
164	Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn		
165	110	115	
166			
167	GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC	585	
168	Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys		
169	120	125	130
170			
171	CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG	624	
172	Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp		
173	135	140	
174			
175	GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC	663	
176	Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala		
177	145	150	155
178			
179	ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC	702	
180	Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr		
181	160	165	170
182			
183	AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG	741	
184	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met		
185	175	180	
186			
187	AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG	780	
188	Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu		
189	185	190	195
190			
191	ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT	819	
192	Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala		
193	200	205	
194			
195	GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA	858	
196	Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro		
197	210	215	220
198			
199	GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT	897	
200	Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro		
201	225	230	235
202			
203	GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC	936	
204	Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile		
205	240	245	

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/096,500DATE: 06/22/98  
TIME: 11:02:01

INPUT SET: S26845.raw

206  
207 ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970  
208 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val  
209 250 255 259  
210  
211 GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020  
212  
213 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070  
214  
215 TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120  
216  
217 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170  
218  
219 AAAAAAAAAA 1180  
220  
221 (2) INFORMATION FOR SEQ ID NO:3:  
222  
223 (i) SEQUENCE CHARACTERISTICS:  
224 (A) LENGTH: 299 amino acids  
225 (B) TYPE: Amino Acid  
226 (D) TOPOLOGY: Linear  
227  
228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
229  
230 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly  
231 -40 -35 -30  
232  
233 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro  
234 -25 -20 -15  
235  
236 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro  
237 -10 -5 1 5  
238  
239 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro  
240 10 15 20  
241  
242 Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro  
243 25 30 35  
244  
245 Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly  
246 40 45 50  
247  
248 Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala  
249 55 60 65  
250  
251 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn  
252 70 75 80  
253  
254 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln  
255 85 90 95  
256  
257 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln  
258 100 105 110

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/096,500**

DATE: 06/22/98  
TIME: 11:02:02

*INPUT SET: S26845.raw*

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Error

Original Text